

Introduction to genetics of subpolar fish and invertebrates

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This 20th Wakefield Symposium, ‘The genetics of subpolar fish and invertebrates’, is the successor of the 11th Wakefield Symposium, ‘Genetics of subarctic fish and shellfish’, which was held in Juneau, Alaska in 1993. In the introduction to that symposium (Gharrett & Smoker 1994), it was noted that: ‘beginning in the 1960s, modern tools of genetic analysis began to be broadly applied in fisheries science’, and that ‘within the past decade (referring to the 1980s), fisheries genetics had entered the mainstream of fisheries resource utilization’. That observation may be an understatement in today’s world of fisheries science. Once-vigorous fisheries in many parts of the world have failed, growing demand for fisheries products has led to full utilization of many remaining capture resources and is driving an increase in aquaculture productivity, and the role of aquaculture has increased dramatically (FAO 2002). Looming over concerns of lost stocks and persistent erosion of genetic variability are predictions of global warming, which may further tax genetic resources. One of the consequences of these developments is an increased interest in and reliance on genetic applications to

many aspects of fisheries management, aquaculture, and conservation.

In addressing those concerns, fisheries scientists have increased their attention to the genetics of fish and fish populations; the number of fish genetics citations has increased fourfold in the last decade (Figure 1). In addition to the increased attention, the application of sophisticated genetic analysis tools, such as studies of mitochondrial DNA (mtDNA) and microsatellites, have nearly caught up with the more traditional allozyme studies in annual citations (Figure 1).

One of the predominant themes of both symposia was the descriptive study of population structure. Descriptive studies are an important step in developing management or conservation plans because they can provide markers for use in stock identification programs and because they can identify distinct productivity units (the geographical scale of such units) in species that do not have convenient or obvious geographical boundaries, such as many marine species. Analyses of allozyme variation, which dominated early fisheries genetics research, still provide valuable

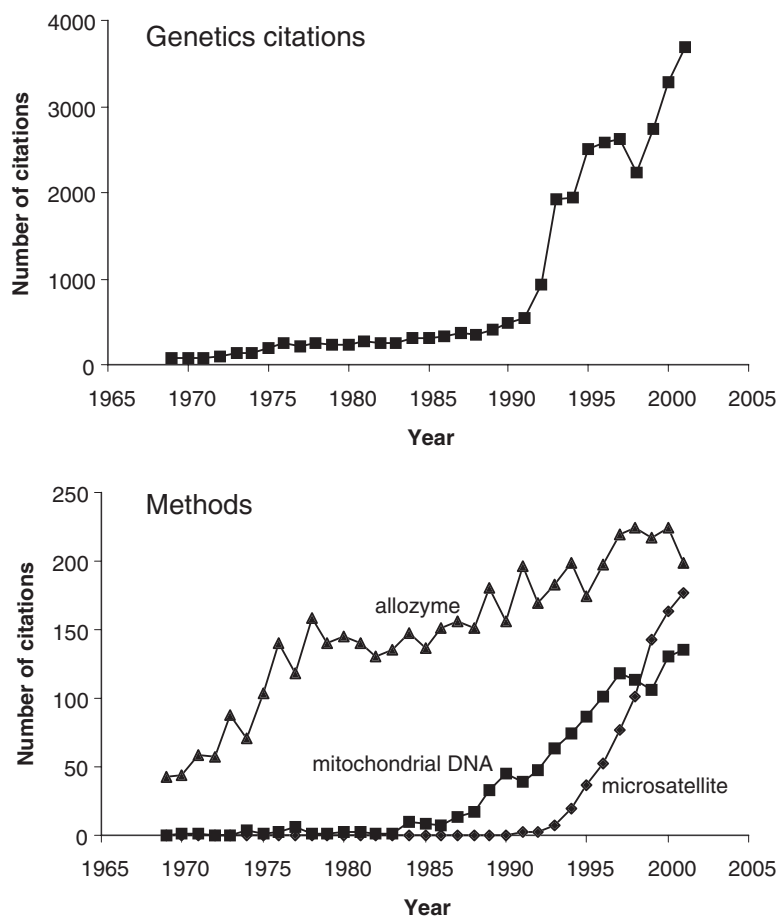


Figure 1. The number of genetics citations from a search of BIOSIS® using combinations of the words and terms (pisces, osteichthyes, or fish) and (genetics or cytogenetics or mtDNA or allozyme or electrophoresis or microsatellite) for papers published each year from 1969 to 2001 (upper). The number of citations for specific molecular methods from a search of BIOSIS Previews (BIOSIS 2001) using combinations of the words and terms (pisces, osteichthyes, or fish) with (1) mtDNA or mitochondrial DNA for mtDNA analyses, (2) allozyme or electrophoresis for allozyme analyses, or (3) microsatellite for microsatellite analyses in papers published each year from 1969 to 2001 (lower). BIOSIS® Previews, BIOSIS, Philadelphia, PA. 20 May 2001. <http://www.biosis.org>.

information and are represented here by studies on Pacific salmon (*Oncorhynchus* spp.; Seeb et al. 2004; Guthrie & Wilmot 2004), herring (*Clupea herengus* and *Clupea pallasii*; Jorstad 2004) and Pacific hake (*Merluccius productus*; Iwamoto et al. 2004). However, descriptive studies increasingly use analyses of DNA variation (Figure 1), particularly mtDNA polymorphisms (Brykov et al. 2004; Sato et al. 2004) and microsatellite variation (Beacham et al. 2004; Curry et al. 2004; Habicht et al. 2004; Matala et al. 2004; Shubina et al. 2004; Wennevik et al. 2004; Young et al. 2004a,b). Some studies combine analyses of allozyme, mtDNA, and microsatellite variation (Jorstad et al.

2004; Thrower et al. 2004). In the last decade, there has also been increased attention to marine species (Brykov et al. 2004; Jorstad 2004; Jorstad et al. 2004; Iwamoto et al. 2004; Matala et al. 2004; Shubina et al. 2004) and focus on finer levels of genetic structure (Curry et al. 2004; Habicht et al. 2004; Thrower et al. 2004; Young et al. 2004a,b).

As geneticists address more complicated – and more interesting – questions, descriptive studies are becoming increasingly sophisticated. A.R. Templeton's keynote address presented an approach to descriptive studies that uses the temporal information inherent in gene and haplotype trees in combination with the

geographical distribution of the genes to make rigorous inferences about historical demographic events that shaped the current distribution. The marriage of phylogenetic information to population genetics promises to provide important insights from studies of fish and invertebrate resources.

One of the genetic applications to fisheries management is the resolution of stock mixtures. These methods have proved useful in a variety of applications including forensics (Withler et al. 2004a). Preliminary studies of high seas distributions of chum salmon (*Oncorhynchus keta*) is extending our knowledge of their biology (Seeb et al. 2004). The analytical basis of this process continues to be developed and refined (Guinand et al. 2004; Olsen et al. 2004; Reynolds & Templin 2004), and data from new descriptive studies must be examined for their suitability for application to specific management issues (Beacham et al. 2004).

The genetic composition of a population is molded from the evolutionary forces and stochastic events that have acted on it. Population differences can emerge from subtle local differences and from random drift, and isolated populations may accrue substantially different genetic architectures, which can be studied using genetic analysis. Consequently, genetics can be used to address a variety of biological questions ranging from elucidating complex mating systems (Seamons et al. 2004; Withler et al. 2004b) to resolving the phenotypic differences among coho populations that involve embryo development and timing (Granath et al. 2004). The differences in genetic architecture among populations take on additional implications in the context of stock transfers that can accompany hatchery, stock enhancement, and aquaculture programs. In addition, artificial culture practices can reduce variability in cultured stocks (Kim et al. 2004). One of the consequences of introgression of transplanted fish is outbreeding depression, which was documented in pink salmon (*Oncorhynchus gorbuscha*) (Gilk et al. 2004). It is likely that steelhead (*Oncorhynchus mykiss*) repeatedly stocked into the Great Lakes contribute their genes to naturally spawning populations (Bartron & Scribner 2004); but, in contrast, the reproductive success of hatchery steelhead in Washington appears to be lower than that of naturally spawning steelhead (McLean et al. 2004). Various measures, including supplementation programs, have been initiated to address the drastic declines in chinook salmon returns that the Columbia River system has experienced in the last century. Detecting stressors while they are occurring,

rather than after the fact, would reduce the time needed by managers to detect and possibly circumvent negative effects. One approach may be detection of decreased embryological developmental stability, which might be indexed by increases in asymmetry of paired structures (like left and right pectoral fin rays) in fish (Johnson et al. 2004). One result of the stressors may be sex conversion, as suggested by the large number of Columbia River system chinook salmon females that carry what were previously presumed to be male-specific markers (Chowen & Nagler 2004).

Several reports involve diverse aquacultural applications. Among the challenges to aquacultural enterprises are disease outbreaks and a need for nutritious, inexpensive diets. In some instances, domesticated stocks can be selected for fish that possess characteristics that are desirable in intensive culture. Resistance to infectious hematopoietic necrosis virus was examined in genes of the major histocompatibility complex of Atlantic salmon (*Salmo salar*) (Miller et al. 2004); and the potential of using variation in gene expression (detected by real-time PCR) to direct selection for growth was also explored (Overturf et al. 2004). In addition, success in increasing the sperm motility of sex-reversed male rainbow trout (*O. mykiss*) will improve the culture of all-female lines (Kobayashi et al. 2004). In what undoubtedly reflects an important future direction for many aspects of fisheries biology and genetics, quantitative trait loci for several meristic traits were detected and examined in rainbow trout (Nichols et al. 2004).

Genetic differences within and between species provide phylogenetic characters that can be used to learn about the demographic history of a species (Templeton 2004), resolve subspecies or species differences (Frolov & Frolova 2004; Oleinik et al. 2004; Templeton 2004), or develop phylogenies for taxa that include numerous species (Phillips et al. 2004). Several different genetic methods were used in phylogenetic applications, including karyotypes (Frolov & Frolova 2004) and mtDNA (Oleinik et al. 2004) in chars (*Salvelinus* spp.), DNA sequences of growth hormone introns in Salmoninae (Phillips et al. 2004), transferrin sequences in brown trout (*Salmo trutta*) species complex (Templeton 2004), and microsatellite flanking sequences in rockfish (*Sebastes* spp.) (Asahida et al. 2004).

In aggregate, these papers reflect questions that are important to modern fisheries science and genetics and,

in comparison to the science presented at the 11th Wakefield Symposium, illustrate the evolution of the field over the past decade. The improved technology will continue to provide tools to address increasingly complicated problems not only in traditional applications but also in ecological and behavioral studies. The union between molecular and quantitative genetics, where many of the major questions about population structure and evolution remain unanswered, will also benefit from the new technologies.

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